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1653

P#13

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/403,861A

DATE: 01/08/2001
 TIME: 15:12:03

Input Set : A:\Riccardi1.txt
 Output Set: N:\CRF3\01082001\I403861A.raw

ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: RICCARDI, Carlo
 8 (ii) TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL
 9 DEATH PATHWAYS

11 (iii) NUMBER OF SEQUENCES: 15

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
 15 (B) STREET: 624 Ninth Street, N.W., Suite 300
 16 (C) CITY: Washington
 17 (D) STATE: D.C.
 18 (E) COUNTRY: USA
 19 (F) ZIP: 20001

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk
 23 (B) COMPUTER: IBM PC compatible
 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/403,861A
 C--> 29 (B) FILING DATE: 11-Feb-2000

C--> 35 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: PCT/EP98/02490
 33 (B) FILING DATE: 27-APR-1998
 36 (A) APPLICATION NUMBER: EP 97107033.9
 37 (B) FILING DATE: 28-APR-1997

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: YUN, Allen C.
 41 (B) REGISTRATION NUMBER: 37,971
 42 (C) REFERENCE/DOCKET NUMBER: RICCARDI=1

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: 202-628-5197
 46 (B) TELEFAX: 202-737-3528

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 1972 base pairs
 53 (B) TYPE: nucleic acid
 54 (C) STRANDEDNESS: single
 55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: cDNA

59 (iii) HYPOTHETICAL: NO

61 (iv) ANTI-SENSE: NO

63 (ix) FEATURE:

64 (A) NAME/KEY: CDS

C--> 65 (B) LOCATION: 206..616

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

69 CTGGCTGCTG TGGAGTTTGT GACATACTAG GTGACACCCT TGGAGTCACT TCTCTTCAAC

60

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Input Set : A:\Riccardil.txt

Output Set: N:\CRF3\01082001\I403861A.raw

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71 TCCAGCTTAG AAGTGCCTGC CTGGCTCAGG GTCGCACTG CAGCCTACTC CTTGCTTCAG 120
73 GGCCTGACTG CAACGCCAAA GCCTATCCTA TACCGGCAGC GCCAGCAGCC ACTCAAACCA 180
75 GCCACAGCTC CCCGGCAACC GAACC ATG AAC ACC GAA ATG TAT CAG ACC CCC 232
76                                     Met Asn Thr Glu Met Tyr Gln Thr Pro
77                                     1                               5
79 ATG GAG GTG GCC GTC TAT CAG CTG CAC AAT TTC TCC ACC TCC TTC TTT 280
80 Met Glu Val Ala Val Tyr Gln Leu His Asn Phe Ser Thr Ser Phe Phe
81 10                               15                               20                               25
83 TCT TCT CTG CTT GGA GGG GAT GTG GTT TCC GTT AAA CTG GAT AAC AGT 328
84 Ser Ser Leu Leu Gly Gly Asp Val Val Ser Val Lys Leu Asp Asn Ser
85                               30                               35                               40
87 GCC TCC GGA GCC AGT GTG GTG GCC CTA GAC AAC AAG ATT GAG CAG GCC 376
88 Ala Ser Gly Ala Ser Val Val Ala Leu Asp Asn Lys Ile Glu Gln Ala
89                               45                               50                               55
91 ATG GAC CTC GTG AAG AAC CAC CTG ATG TAC GCT GTG AGA GAG GAG GTG 424
92 Met Asp Leu Val Lys Asn His Leu Met Tyr Ala Val Arg Glu Glu Val
93 60                               65                               70
95 GAG GTC CTA AAG GAG CAG ATT CGT GAG CTG CTT GAG AAG AAC TCC CAG 472
96 Glu Val Leu Lys Gln Gln Ile Arg Glu Leu Leu Glu Lys Asn Ser Gln
97 75                               80                               85
99 CTG GAG CGC GAG AAC ACC CTC CTG AAG ACG CTG GCA AGC CCC GAG CAA 520
100 Leu Glu Arg Glu Asn Thr Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln
101 90                               95                               100                               105
103 CTG GAA AAG TTC CAG TCC CGG CTG AGC CCT GAA GAG CCA GCA CCT GAA 568
104 Leu Glu Lys Phe Gln Ser Arg Leu Ser Pro Glu Glu Pro Ala Pro Glu
105                               110                               115                               120
107 GCC CCA GAA ACC CCG GAA ACC CCG GAA GCC CCT GGT GGT TCT GCG GTG 616
108 Ala Pro Glu Thr Pro Glu Thr Pro Glu Ala Pro Gly Gly Ser Ala Val
109                               125                               130                               135
111 TAAGTGCTC TGTCCTTAGG GTGGGCAGAG CCACATCTTG TTCTACCTAG TTCTTTCCAG 676
113 TTTGTTTTTG GCTCCCAAG GGTCACTCA TGTGGAGAAC TTACACCTA ACATAGCTGG 736
115 TGCCAAGAGA TGTCCTTAGG ACATGCCCAT CTGGGTCCAC TCCAGTGACA GACCCCTGAC 796
117 AAAGAGCAGG TCTCTGGAGA CTAAGTTGCA TGGGGCCTAG TAACACCAAG CCAGTGAGCC 856
119 TGTCGTGTCA CCGGGCCCTG GGGGCTCCCA GGGCTGGGCA ACTTAGTTAC AGCTGACCAA 916
121 GGAGAAAGTA GTTTTGAGAT GTGATGCCAG TGTGCTCCAG AAAGTGTAAG GGGTCTGTTT 976
123 TTCATTTCCA TGGACATCTT CCACAGCTTC ACCTGACAAT GACTGTCCT ATGAAGAAGC 1036
125 CACTGTGTGT CTAAGCAGAA GCAACCTCTC TCTTCTTCCT CTGTCTTTTC CAGGCAGGGG 1096
127 CAGAGATGGG AGAGATTGAG CCAAATGAGC CTTCTGTTGG TTAATACTGT ATAATGCATG 1156
129 GCTTTGTGCA CAGCCCACTG TGGGGTTACA GCTTTGGGAT GACTGCTTAT AAAGTTCTGT 1216
131 TTGGTTAGTA TTGGCATCGT TTTTCTATAT AGCCATAATG CGTATATATA CCCATAGGGC 1276
133 TAGATCTATA TCTTAGGTA GTGATGTATA CATATACACA TACACCTACA TGTGAAGGG 1336
135 CCTAACACAG TTTGGGAGTA CTGACTGGTC TCTTATCTCT TAAAGCTAAG TTTTTCAGTG 1396
137 TGCTAATTTA CCAAATTGAT CCAGTTTGTC CTTTATAGTA AATAAGACTC GATATGAGGG 1456
139 AGGGAGGGGA AGACAGCCT CACAATGCGG CCACAGATGC CTTGCTGCTG CAGTCCCTCC 1516
141 TGATCTGTCC ACTGAAGACA TGAAGTCCTC TTTTGAATGC CAAACCCACC ATTCATGGGT 1576
143 CCGTACTACA TAGAATGGGG TTGAGAGAAG ATCAGTTTGG ACTTCACATT TTTGTTTAA 1636
145 GTTTTAGGTT GTTTTGTGTT GGTGTTGTTT GTTTGTTGTT TGTGTTGTTT TGTGTTTGTG 1696
147 TTTTCTTTT TTAAGTTCTT GTGGGAAAC TTTGGGGTTA ATCAAAGGAT GTAGTCCTGT 1756
149 GGTAGACCAG AGGAGTAACT AGTTTGTATC CTTTGGGGTG TGGAAATGT ACCCAGGAAG 1816

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 PATENT APPLICATION: US/09/403,861A TIME: 15:12:03

Input Set : A:\Riccardil.txt
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151 CTTGTGTAAG GAGGTTCTGT GACAGTGAAC ACTTTCCTACT TTCTGACACC TCATCCTGCT 1876
 153 GTACGACTCC AGGATTTCGA TTTCGATTTT TCAAATGTAG CTGGAATTT CAATAAACTT 1936
 155 TGCTCCTTTT TCTAAAAATA AAAAAAAAAA AAAAAA 1972
 158 (2) INFORMATION FOR SEQ ID NO: 2:
 160 (i) SEQUENCE CHARACTERISTICS:
 161 (A) LENGTH: 137 amino acids
 162 (B) TYPE: amino acid
 163 (D) TOPOLOGY: linear
 165 (ii) MOLECULE TYPE: protein
 167 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 169 Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln
 170 1 5 10 15
 172 Leu His Asn Phe Ser Thr Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp
 173 20 25 30
 175 Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val
 176 35 40 45
 178 Ala Leu Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His
 179 50 55 60
 181 Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu Gln Ile
 182 65 70 75 80
 184 Arg Glu Leu Leu Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu
 185 85 90 95
 187 Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Arg
 188 100 105 110
 190 Leu Ser Pro Glu Glu Pro Ala Pro Glu Ala Pro Glu Thr Pro Glu Thr
 191 115 120 125
 193 Pro Glu Ala Pro Gly Gly Ser Ala Val
 194 130 135
 196 (2) INFORMATION FOR SEQ ID NO: 3:
 198 (i) SEQUENCE CHARACTERISTICS:
 199 (A) LENGTH: 20 base pairs
 200 (B) TYPE: nucleic acid
 201 (C) STRANDEDNESS: single
 202 (D) TOPOLOGY: linear
 204 (ii) MOLECULE TYPE: cDNA
 206 (iii) HYPOTHETICAL: NO
 208 (iv) ANTI-SENSE: NO
 210 (ix) FEATURE:
 211 (A) NAME/KEY: misc_feature
 212 (B) LOCATION:1..20
 213 (D) OTHER INFORMATION:/note= "PCR forward primer"
 215 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 217 CCATCTGGGT CCACTCCAGT 20
 219 (2) INFORMATION FOR SEQ ID NO: 4:
 221 (i) SEQUENCE CHARACTERISTICS:
 222 (A) LENGTH: 20 base pairs
 223 (B) TYPE: nucleic acid
 224 (C) STRANDEDNESS: single
 225 (D) TOPOLOGY: linear

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227      (ii) MOLECULE TYPE: cDNA
229      (iii) HYPOTHETICAL: NO
231      (ix) FEATURE:
232          (A) NAME/KEY: misc_feature
233          (B) LOCATION:1..20
234          (D) OTHER INFORMATION:/note= "PCR reverse primer"
236      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
238 AGGACAGTGG GAGTGGCACC
240 (2) INFORMATION FOR SEQ ID NO: 5:
242      (i) SEQUENCE CHARACTERISTICS:
243          (A) LENGTH: 1946 base pairs
244          (B) TYPE: nucleic acid
245          (C) STRANDEDNESS: single
246          (D) TOPOLOGY: linear
248      (ii) MOLECULE TYPE: cDNA
250      (iii) HYPOTHETICAL: NO
252      (iv) ANTI-SENSE: NO
254      (ix) FEATURE:
255          (A) NAME/KEY: CDS
256          (B) LOCATION:241..642
258      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
260 AATTCGGGGG CCGTGGAGTT TGTGACATAC GAGGTGACAC CCCTCGAGTC ACTTCCCTTC
262 AACTCCAGCT GGAGCGCTTG CTTGGCTTTG GGTTCGTTCT GCAGCCTTCG CCCGCTCCT
264 AGCCTCAGGG CCGACTCCA GCGCAGAGCC CAGCCAGCG CAGCCTGCCA GCAGCCACCC
266 AGCCGCCAG CCGCCAGCC CCGCACGAAA CCCGGCCAGA GCTTCCTAGC AGCCCGAGCC
268 ATG AAC ACC GAA ATG TAT CAG ACC CCC ATG GAG GTG GCG GTC TAC CAG
269 Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln
W--> 270      5      10      15
272 CTG CAC AAT TTC TCC ATC TCC TTC TCT TCT CTG CTF GGA GGG GAT
273 Leu His Asn Phe Ser Ile Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp
274      20      25      30
276 GTG GTT TCC GTT AAG CTG GAC AAC AGT GCC TCC GGA GCC AGC GTG GTG
277 Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val
278      35      40      45
280 GCC ATA GAC AAC AAG ATC GAA CAG GCC ATG GAT CTG GTG AAG AAT CAT
281 Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His
282      50      55      60
284 CTG ATG TAT GCT GTG AGA GAG GAG CTG GAG ATC CTG AAG GAG CAG ATC
285 Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile
286      65      70      75      80
288 CGA GAG CTG GTG GAG AAG AAC TCC CAG CTA GAG CGT GAG AAC ACC CTG
289 Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu
290      85      90      95
292 TTG AAG ACC CTG GCA AGC CCA GAG CAG CTG GAG AAG TTC CAG TCC TGT
293 Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys
294      100      105      110
296 CTG AGC CCT GAA GAG CCA GCT CCC GAA TCC CCA CAA GTG CCC GAG GCC
297 Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala
298      115      120      125

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Input Set : A:\Riccardil.txt

Output Set : N:\CRF3\01082001\I403861A.raw

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300 CCT GGT GGT TCT GCG GTG TAAGTGGCTC TGTCTCAGG GTGGGCAGAG 672
301 Pro Gly Gly Ser Ala Val
302 130
304 CCACATAAAT TGTTTTACCT AGTTCTTTCC AGTTTGTFTT TGGCTCCCA AGCATCATCT 732
306 CACGAGGAGA ACTTTACACC TAGCACAGCT GGTGCCAAGA GATGTCTTAA GGACATGGCC 792
308 ACCTGGGTCC ACTCCAGCGA CAGACCCCTG ACAAGAGCAG GTCTCTGGAG GCTGAGTTGC 852
310 ATGGGGCCTA GTAACACCAA GCCAGTGAGC CTCTAATGCT ACTGCGCCCT GGGGGCTCCC 912
312 AGGGGCTGGG CAACCTTAGCT GCAACTGGCA AAGGAGAAGG GTAGTTTGAG GTGTGACACC 972
314 AGTTTGTCTC AGAAAGTTTA AGGGGTCTGT TTCTCATCTC CATGGACATC TTCAACAGCT 1032
316 TCACCTGACA ACGACTGTTT CTATGAAGAA GCCACTTGTG TTTTAAGCAG AGGCAACCTC 1092
318 TCTCTTCTCC TCTGTTTCGT GAAGGCAGGG GACACAGATG GGAGAGATTG AGCCAAGTCA 1152
320 GCCTTCTGTT GGTAAATATG GTATAATGCA TGGCTTTGTG CACAGCCCAG TGTGGGATTA 1212
322 CAGCTTTGGG ATGACCGCTT ACAAGTTCTT GTTTGGTTAG TATTGGCATA GTTTTCTAT 1272
324 ATAGGCATAA ATGCGTATAT ATACCCATAG GCCTAGATCT GTATCTTAGT GTAGCGATGT 1332
326 ATACATATAC ACATCCACCT ACATGTTGAA GGGCCTAACG AGCCTTGGGA GTATTGACTG 1392
328 GTCCCTTACC TCTTATGGCT AAGTCTTTGA CTGTGTTTCA TTACCAAGTT GACCCAGTTT 1452
330 GTCTTTTAGG TTAAGTAAGA ACTCGAGAGT AAAGGCAAGG AGGGGGGCCA GCTCTGAAT 1512
332 GCGGCCACGG ATGCCCTGCT GCTGCAACCC TTTCCCCAGC GTCCACTGA AACGTGAAGT 1572
334 CCTGTTTGA ATGCCAAACC CACCATTCAC TGGTGCTGAC TACATAGAAT GGGTTGAGAG 1632
336 AAGATCAGTT TGGGCTTCAC AGTGTCTATT GAAAAAGCGT TTTTGTTTTG TTTTGAATTA 1692
338 TTGTGGAATA CTTTCAAGTG AACAGAAGGA TGGTGCTCTA CTGTGGATGA GGGATGAACA 1752
340 AGGGGATGGC TTTGATCCAA TGGAGCCTGG GAGGTGTGCC CAGAAAGCTT GTCTGTAGCG 1812
342 GGTTTTGTGA GAGTGAACAC TTTCCACTTT TTGACACCTT ATCCTGATGT ATGGTTCCAG 1872
344 GATTTGGATT TTGATTTTCC AAATGTAGCT TGAAATTTCA ATAAACTTTG CTCTGTTTTT 1932
346 CTAATAAATA AAAA 1946

349 (2) INFORMATION FOR SEQ ID NO: 6:
351 (i) SEQUENCE CHARACTERISTICS:
352 (A) LENGTH: 134 amino acids
353 (B) TYPE: amino acid
354 (D) TOPOLOGY: linear
356 (ii) MOLECULE TYPE: protein
358 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
360 Met Asn Thr Glu Met Tyr Glu Thr Pro Met Glu Val Ala Val Tyr Gln
361 1 5 10 15
363 Leu His Asn Phe Ser Ile Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp
364 20 25 30
366 Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val
367 35 40 45
369 Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His
370 50 55 60
372 Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile
373 65 70 75 80
375 Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu
376 85 90 95
378 Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys
379 100 105 110
381 Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala
382 115 120 125
384 Pro Gly Gly Ser Ala Val

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VERIFICATION SUMMARY DATE: 01/08/2001
PATENT APPLICATION: US/09/403,861A TIME: 15:12:04

Input Set : A:\Riccardil.txt
Output Set: N:\CRF3\01082001\I403861A.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:394 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7, Value=[peptide]